

1101 CCTTCACTC CTCGACCC CTCATGAGGA AGCTGGCCCT CAGGCTCATGAGG TCGCTTAAGG TGAGGCAACCC GGCACACAGG AACACCTCTA
 CGAACCTAG GACCTGGC GACTACTCC TCAACCGGA GTACCTCTTA CTCTATTCV ACAGATTCTG ACTOPCTCCC CGCTCTCCC TGTTGAAACAT
 322 Pheaspse KTPGluPro LeuNtaryL yLeuglyLs uMetAspAln GluIleLysV AlalaLysV alalaLysV alalaLysV alalaLysV
 1201 CACGATGCTG ATTAAGTGG TCAACGAAAC CGGGCGCAT GCCTCTCTCC ACACCTCTGCT GGRTGCTCTG GAGAGCTCG GAGAGAGCT
 CGCTGAC TATTCACCC ACTTCTTTG CGCCGCTATA CGGAGACGG TGTTGGACGA CCTAACGGC CTCCTGCCCC ACGGCTTGTC
 355 ThreMetLeu IleLysTyrV alaLysV alaLysV alaLysV alaLysV alaLysV alaLysV alaLysV alaLysV alaLysV
 1301 AGATTGAGG ACCACTGTG GAGCTCTGG AAGTTCTGT ATCTAGAGG TAATGAGAG TAATGAGAC CCTAAGGCTGT CCTAGGCTG
 TCTTAACCTC TCGTGAACRA CTCGACCT TTCAAGTACA TAGATCTCC ATTACGCTG AGAGGAAAC CCTTCACCT CCTTCACCT
 388 LysIleGlu SphIleLeu userserGLY LysPheMetT yIleuGlugl YASnAlaRBP SerAlaXqq S eFG*
 1401 CCTTCCTCG TTTACCTTT TTCTGGAAA AGCCCACCTG GACTCCAGTC AGTAGGAAAG TGCCACATT GTCACATGAC CGCTACTGGA AGAAAACCTC
 GGAAGGGACC AAATGGAAA AACACCTTT TGGGTCTAC CTAGGTCTAG TCACTCCCTTC ACGGTGTTRA CAGTGTAACG CCTATGACCT TCTTGGAG
 1501 CCATCCACA TCACCCACTG GATGGACAT CCTGTAACCTT TCTACCTCCAC TTGGCATTT TTTTATAGG TGAATGAGT AATAAGGACA CTATGGAAAT
 CGTAGGCTGT AGTGGGTCTAC AACGTACCTAA GGACATCTA CTACCTCTA AACGTACCTG AACATATTG ACTTACACTA TTATTCCTGT GATACTTTA
 1601 GTCGCGATCA TTCCGTTCTG AGATTGCTT GCGTACTCTG AGATTGCTT TGGGATGTCAC TTGTTTCAC ACCACTTTT TATCCTATG TAATGCTT ATTATTTAT
 CGACCTAGT RAGGCAACCA CCTAANCAA ACCCTACAGT AACAAAGCT TCCTGAAAAA ATAGGATTAC ATTACGAAA TAAATTAATA
 1701 TTGGGCTACA TTGTAGATC CATCTACARA AAAAARAAA AAAAAAAAAG GGGGGCCCGG ACTCTAGAGT CGACCTGGCAG AAGCTTGGCC GCCATGGCC
 AACCCGATGT AACATTCTAG GTAGATGTT TTGTTTTTCC CGGGGGCCG TCTGATCTCA CCTGGACGTC TTGGAACCGG CGGTACCGG

Fig. 1 (cont.)

1665 T 600 " DTF Z 916 E 610

Fig. 2 A

1 NEORGONAPASGARKERHGCPREARGAAPPGLRVPKTLVLYVAVLLYSAESALITQOD
61 LAPQQRAAPOQKRSSPSEGICPPGHBTISEDGRDCISCRYGODYSTHEWNDLFCRLCTRD
121 SCEVELSPCTTENTVCOCEFTGTFREDSSPEMCRKCRTCERGMVKVGDCTPWSDIECH
181 KFSGILIGYTVAVLLIVAVFVCKSLLMKVLPYXKGICSGGGDPERVDRSSQPGAEQ
241 RVLNEFVSILOPTQVPEQEMEVQEPAEPTGVNMLSPGESEHILLEPAEERSORRLLVPA
301 NEGDEPTETLROCFDDFAFLVTFDSWEPLMRKIGLMNEIKVAKAFAGHDLTLYTMLIKW
361 VAKTGCRDASVETLLDALETLGEFLAKQKIEDHLLSGKFMYLEGNADSALS

Fig. 2 B

Apo2
DR4
APO3/DR3
TNFR1
Fas/Apol

Apo2
DR4
APO3/DR3
TNFR1
Fas/Apol

065750 "DTZ962600

Fig. 3

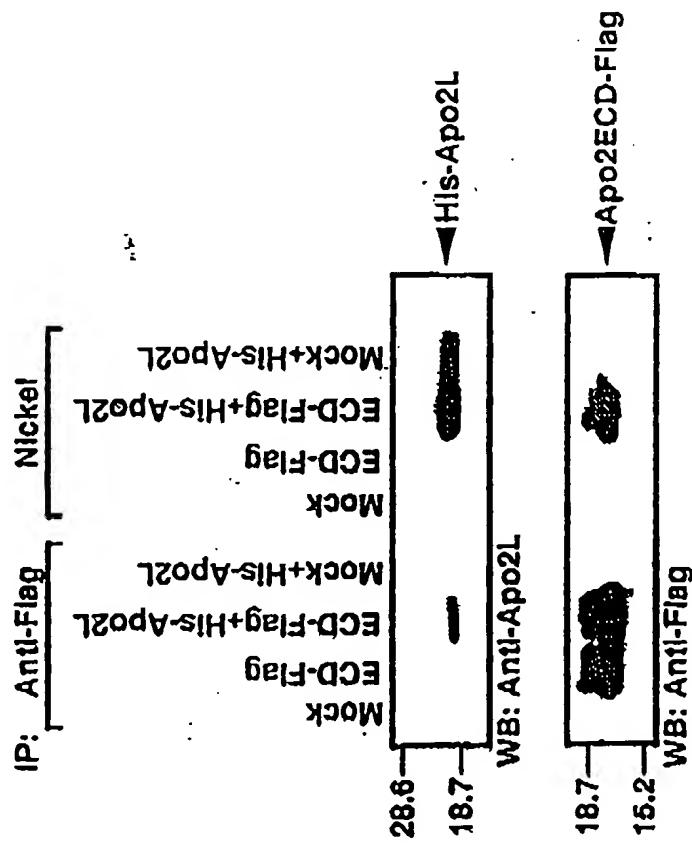
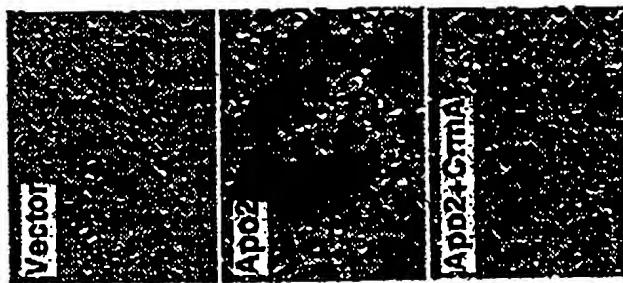


Fig. 4

6.6 5.5 4.5 3.5 2.5 1.5 0.0

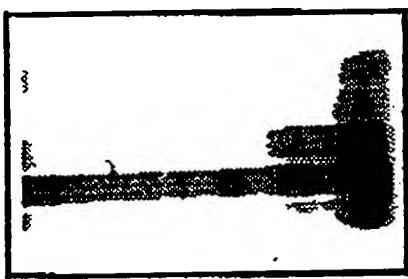
4 A



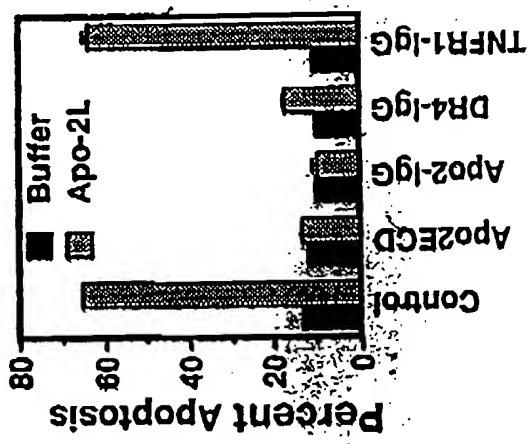
4 C



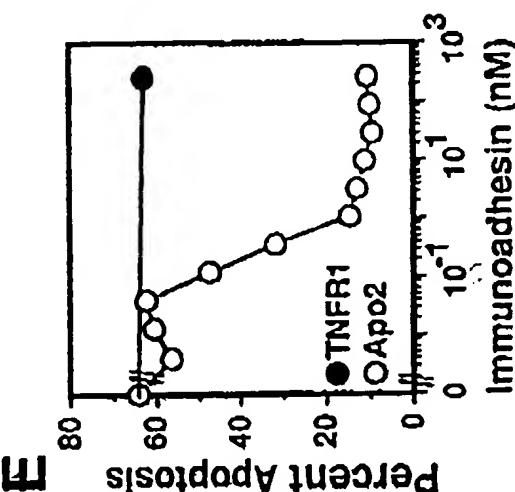
4 B



4 D



4 E



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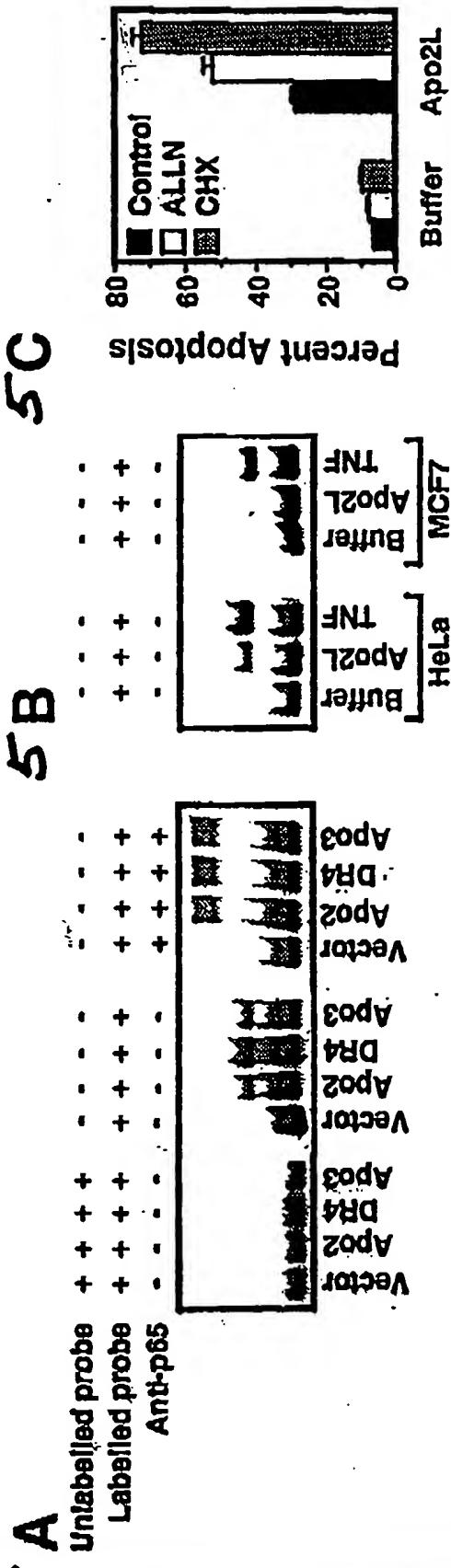
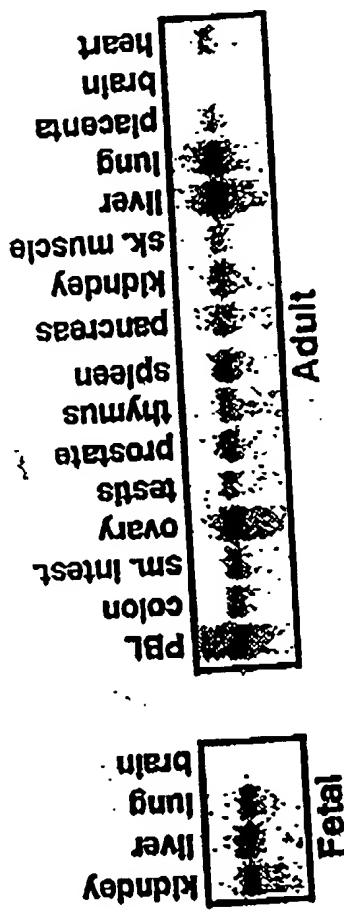


Fig. 6



55555555555555555555555555555555

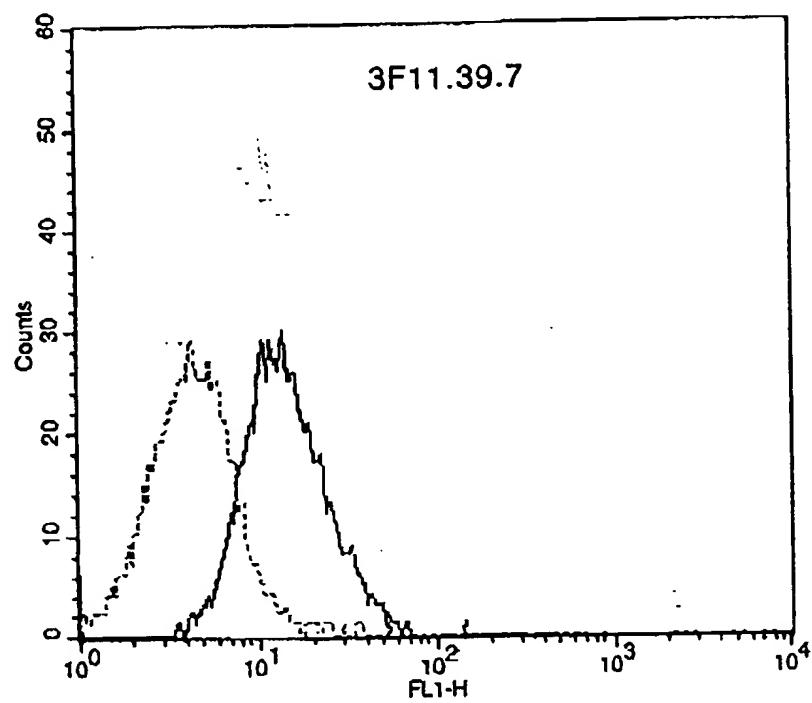


Fig. 7

Dose response curve

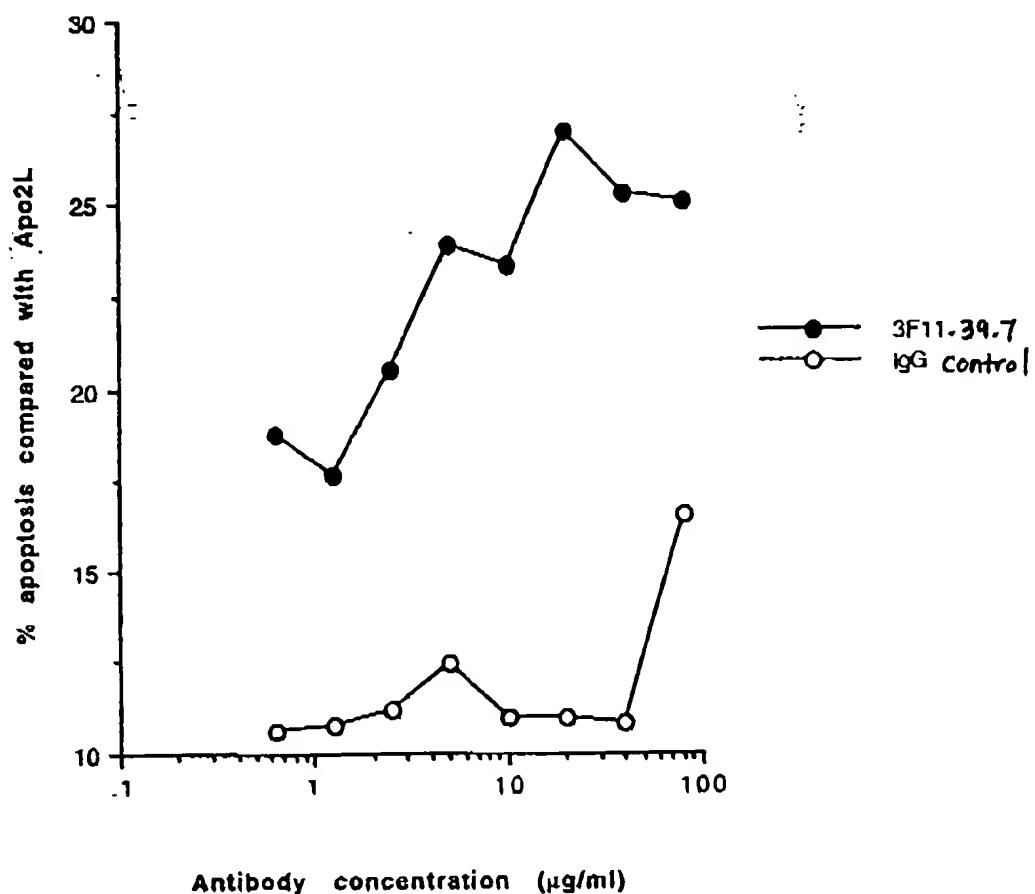


Fig. 8

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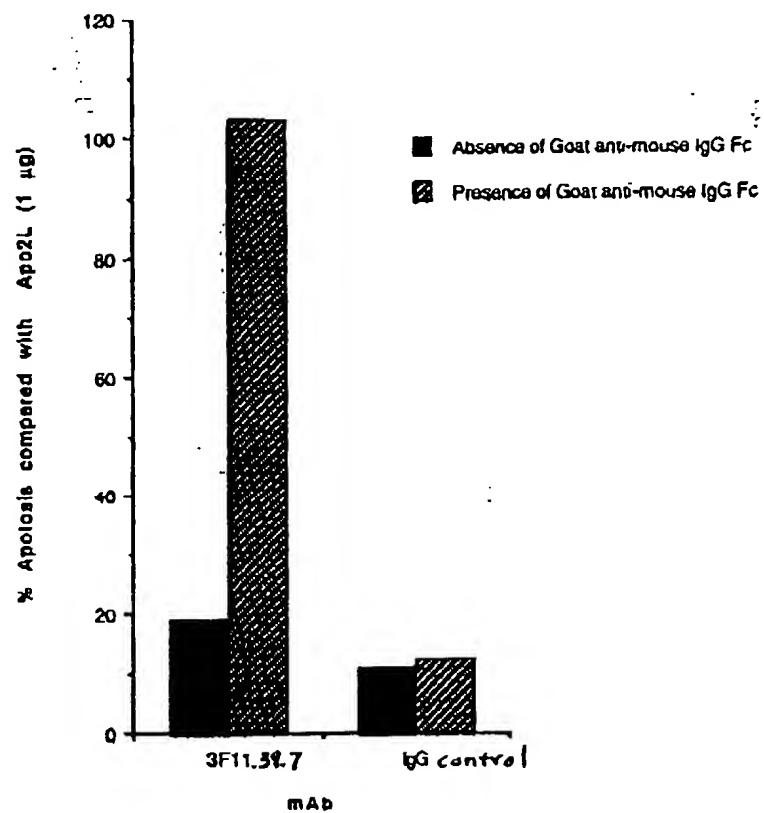


Fig. 9

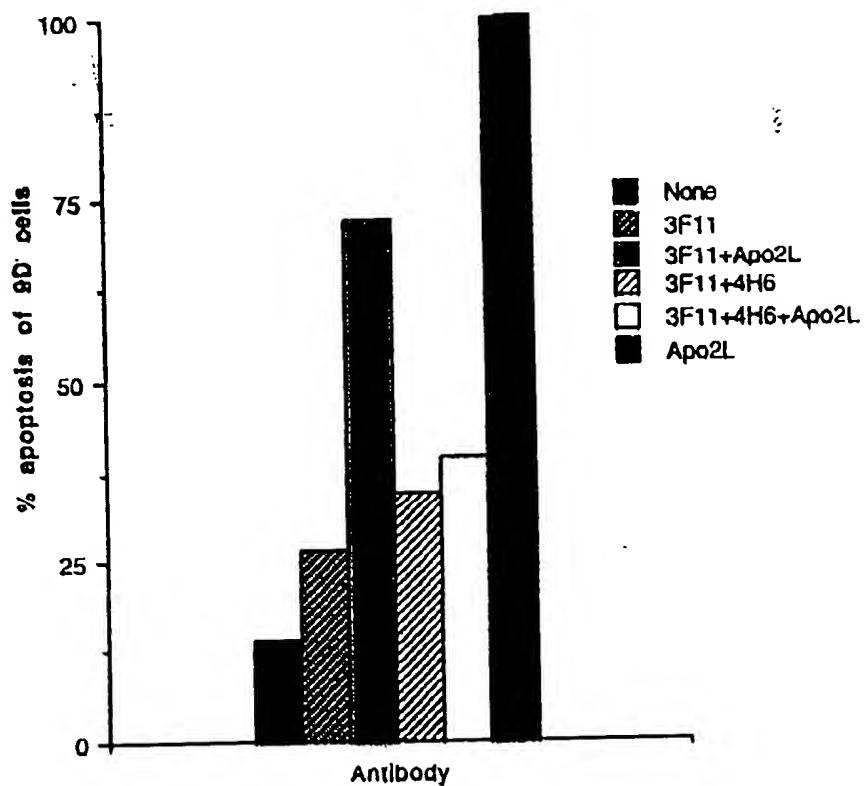


Fig : 10

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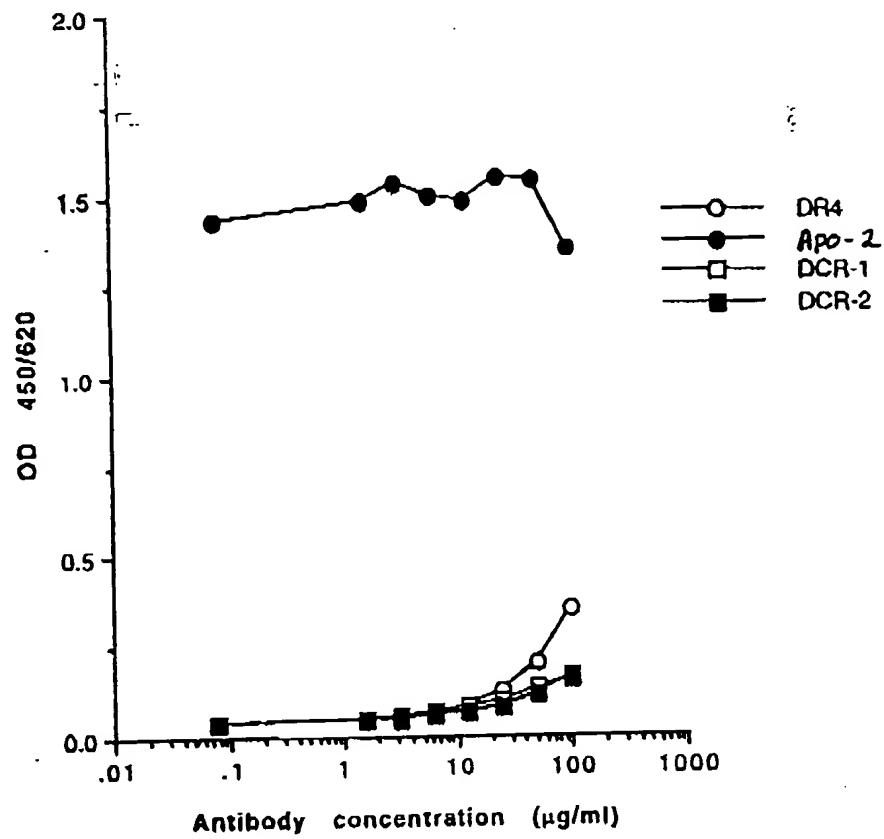


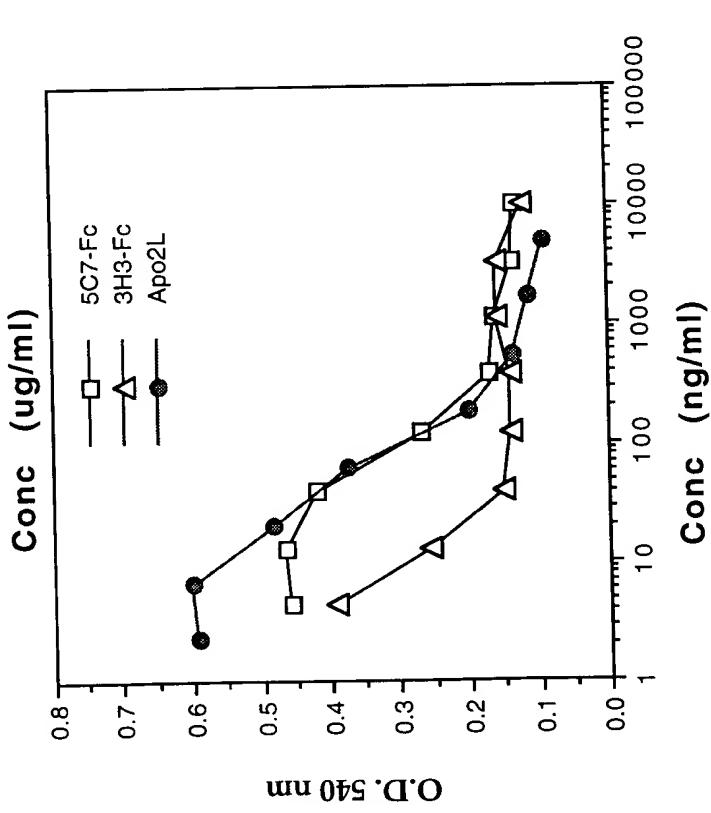
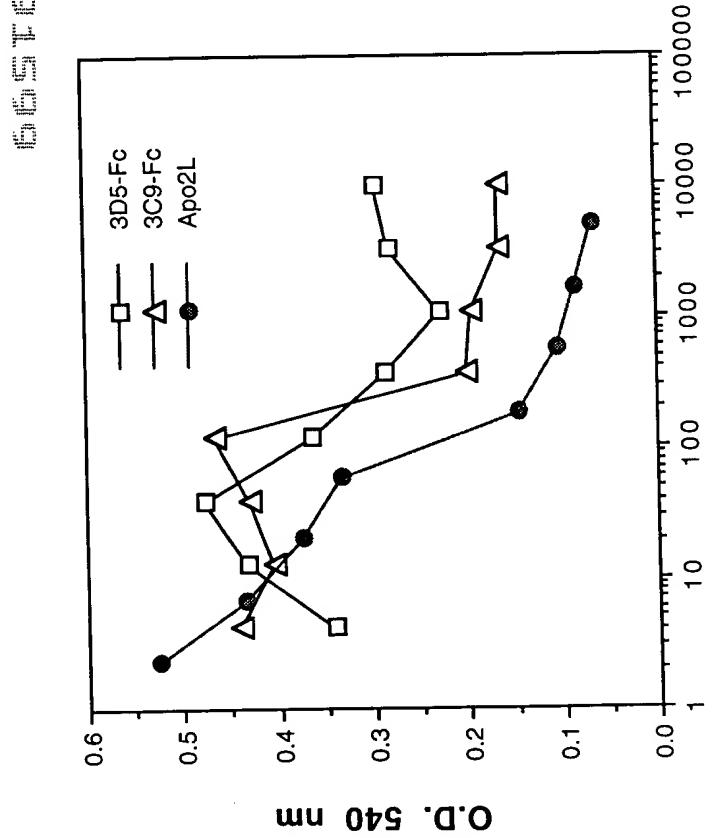
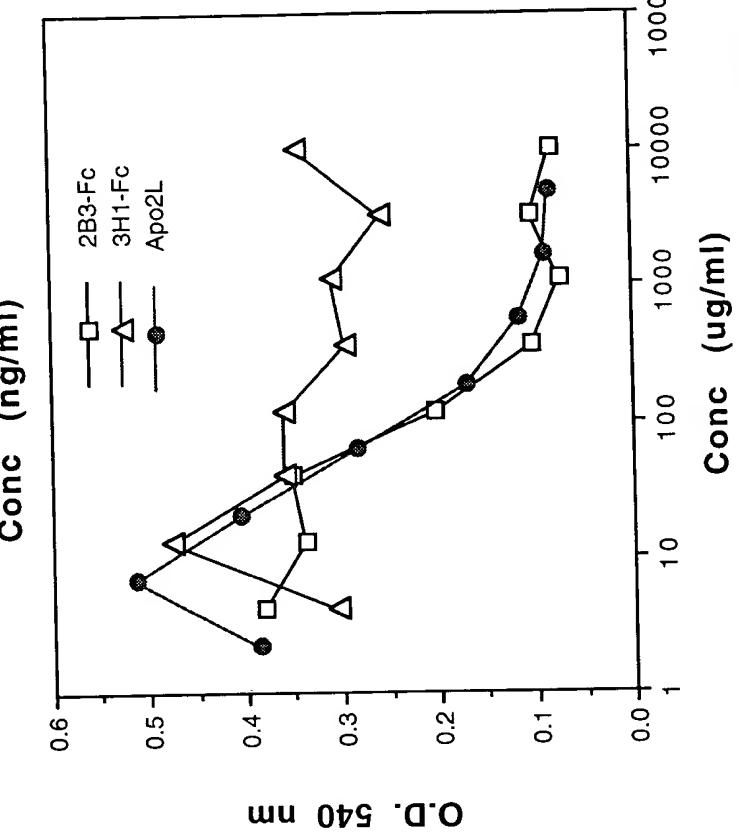
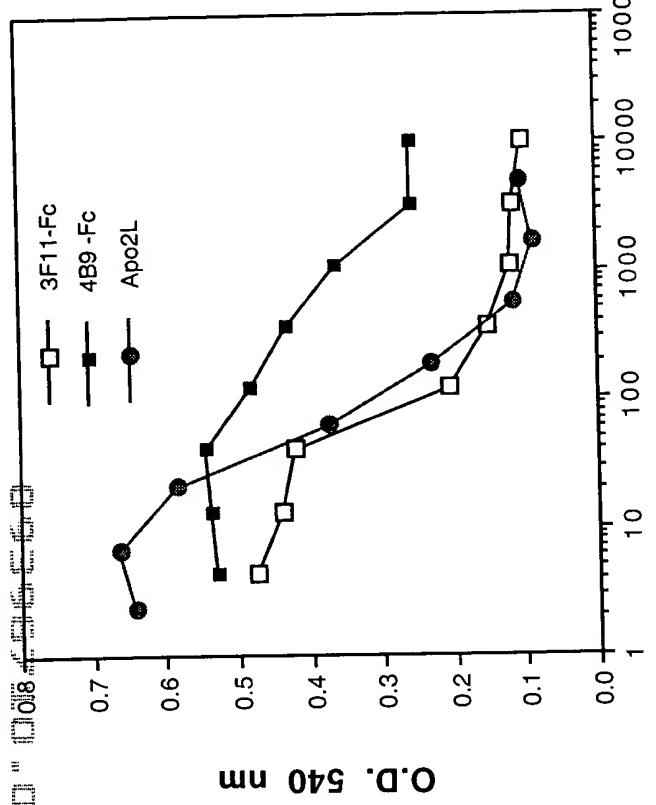
Fig. 11

Fig. 12

Isotype	Kd-1 (pM)	Bloc	Apop w/L	Cross reactivity				IHC
				DR4	$A_{\rho\alpha-\omega}$	DCR1	DCR2	
2B3.7.1	IgG1	-	+	++	-	-	-	+
3F11.39.7	IgG1	20.	+	-	++	-	-	-
4B9.23.6	IgG2a	-	+/-	-	++	-	-	-
5C7.9.1	IgG1	-	+	+	++	-	-	-
3H1.18.10	IgG1	-	-	+	++	-	+/-	+
3H3.14.5	IgG1	4	+	+	++	+	+/-	+
3D5.1.10	IgG1	-	+	++	++	-	-	-
3C9.8.6	IgG2b	+	?	-	++	-	-	-
4H10.14.10	IgG2a	+/-	+/-	++	++	+/-	+/-	-

		Affinity (pM)
DR4-IgG	to Apo2L	82
Apo-2 -IgG	to Apo2L	1
mAb 3F11	to Apo-2 IgG	20
mAb 3H3	to "	3

Fig. 13



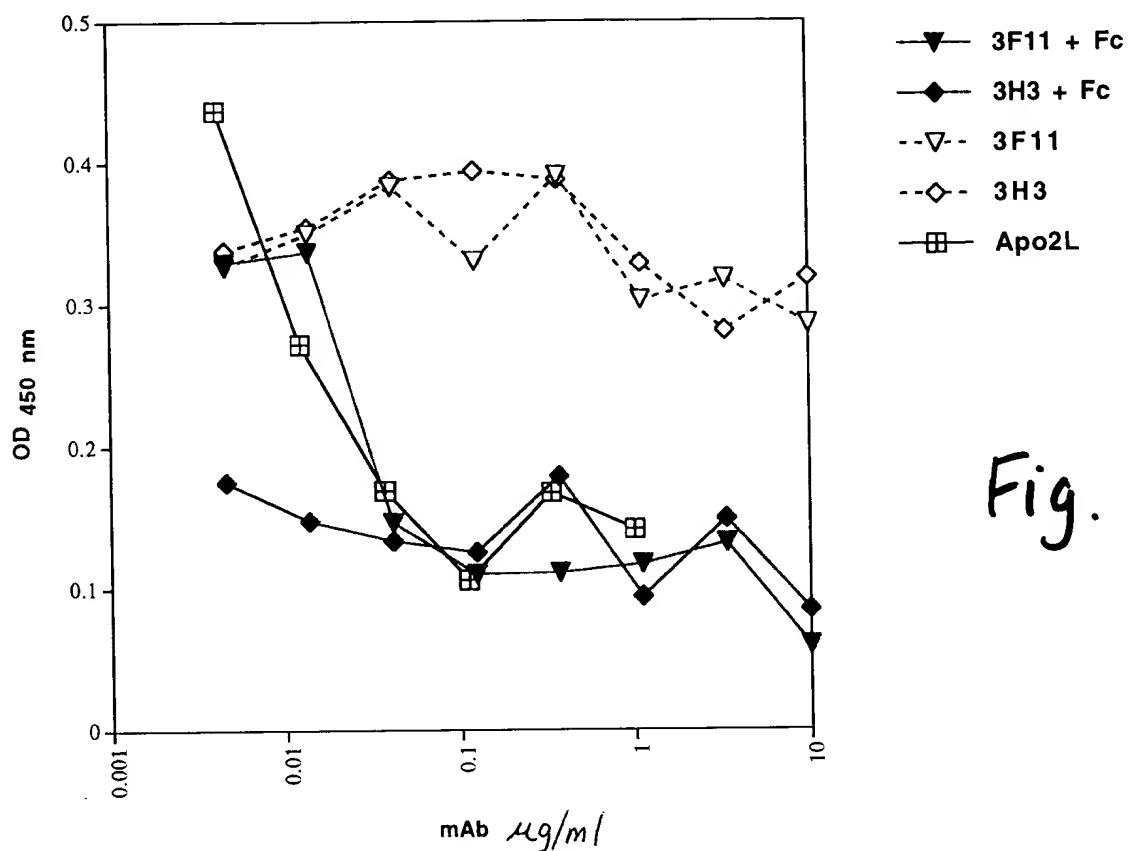


Fig. 15A

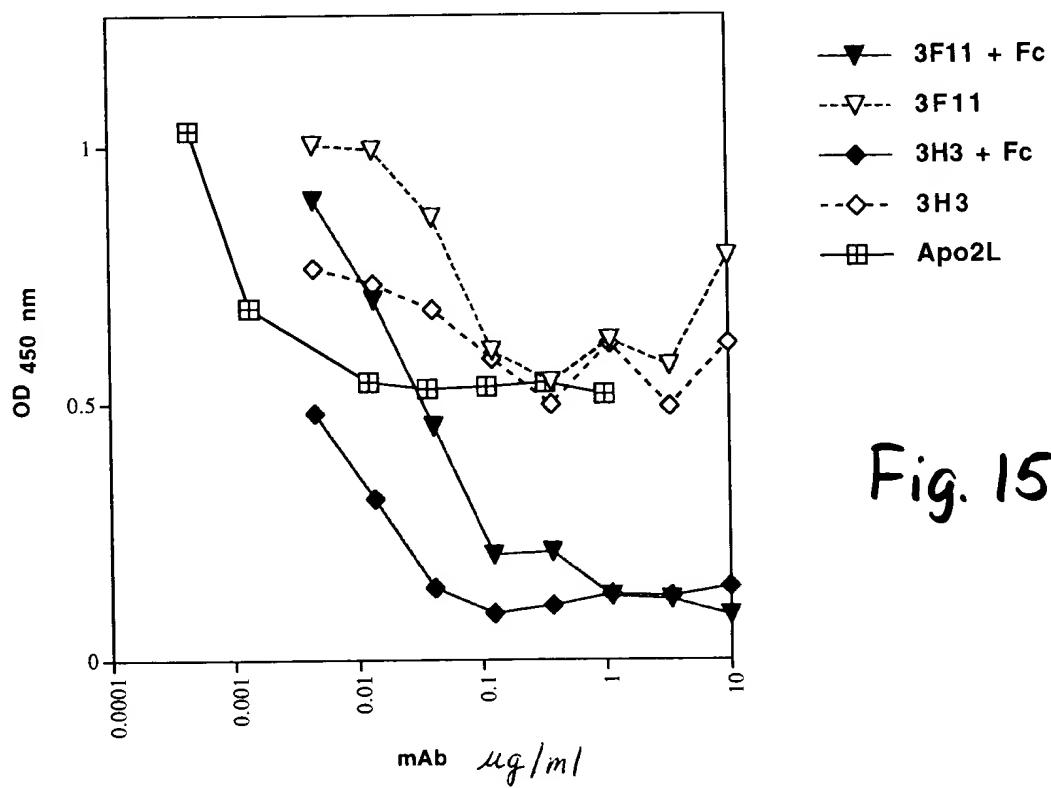


Fig. 15B

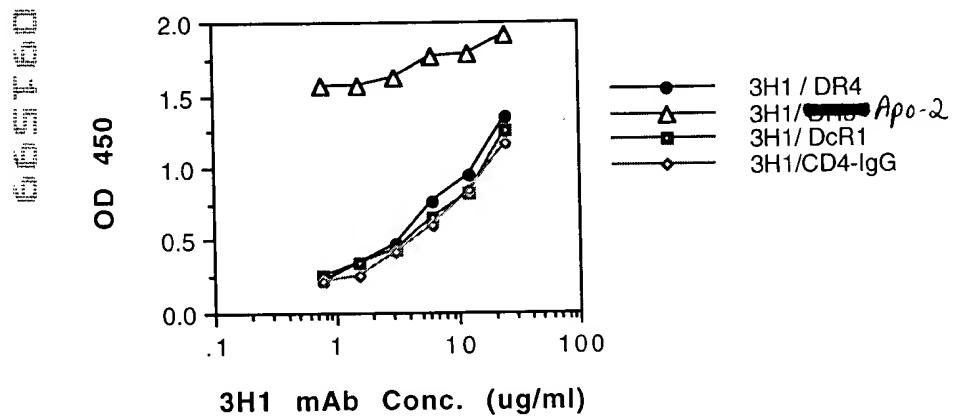
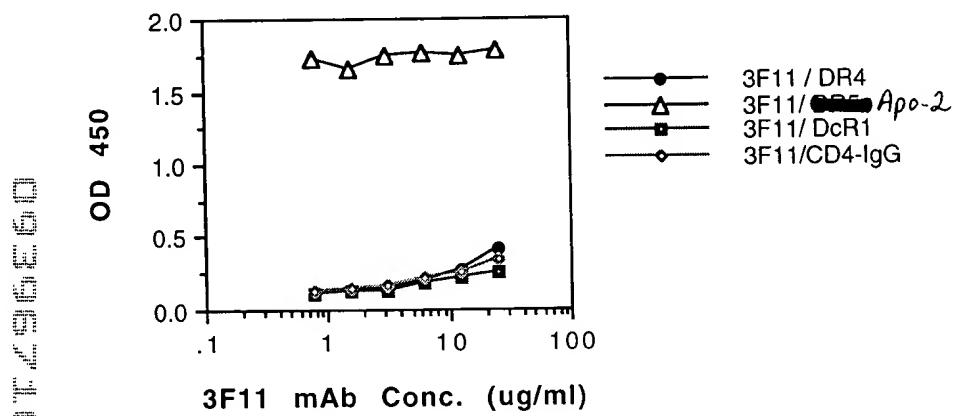
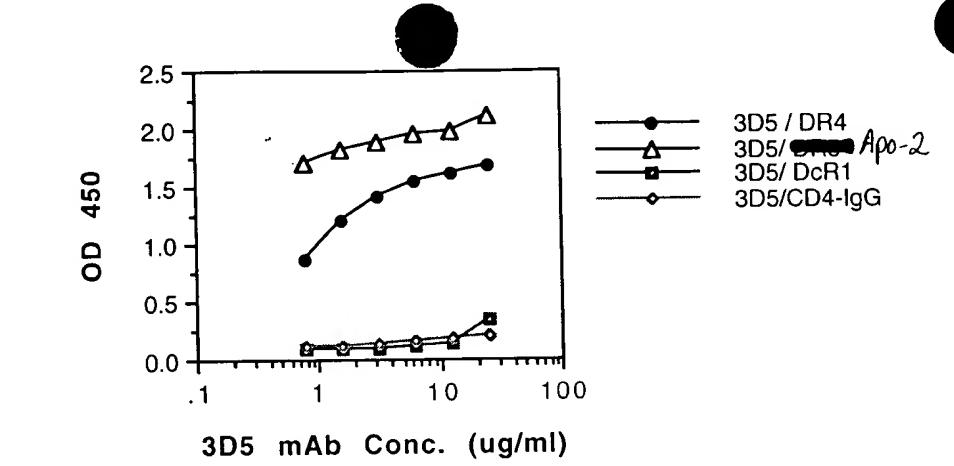
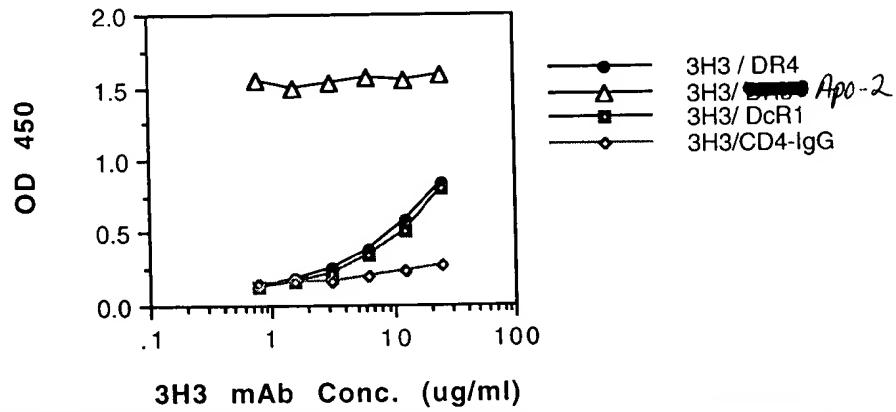


Fig. 16



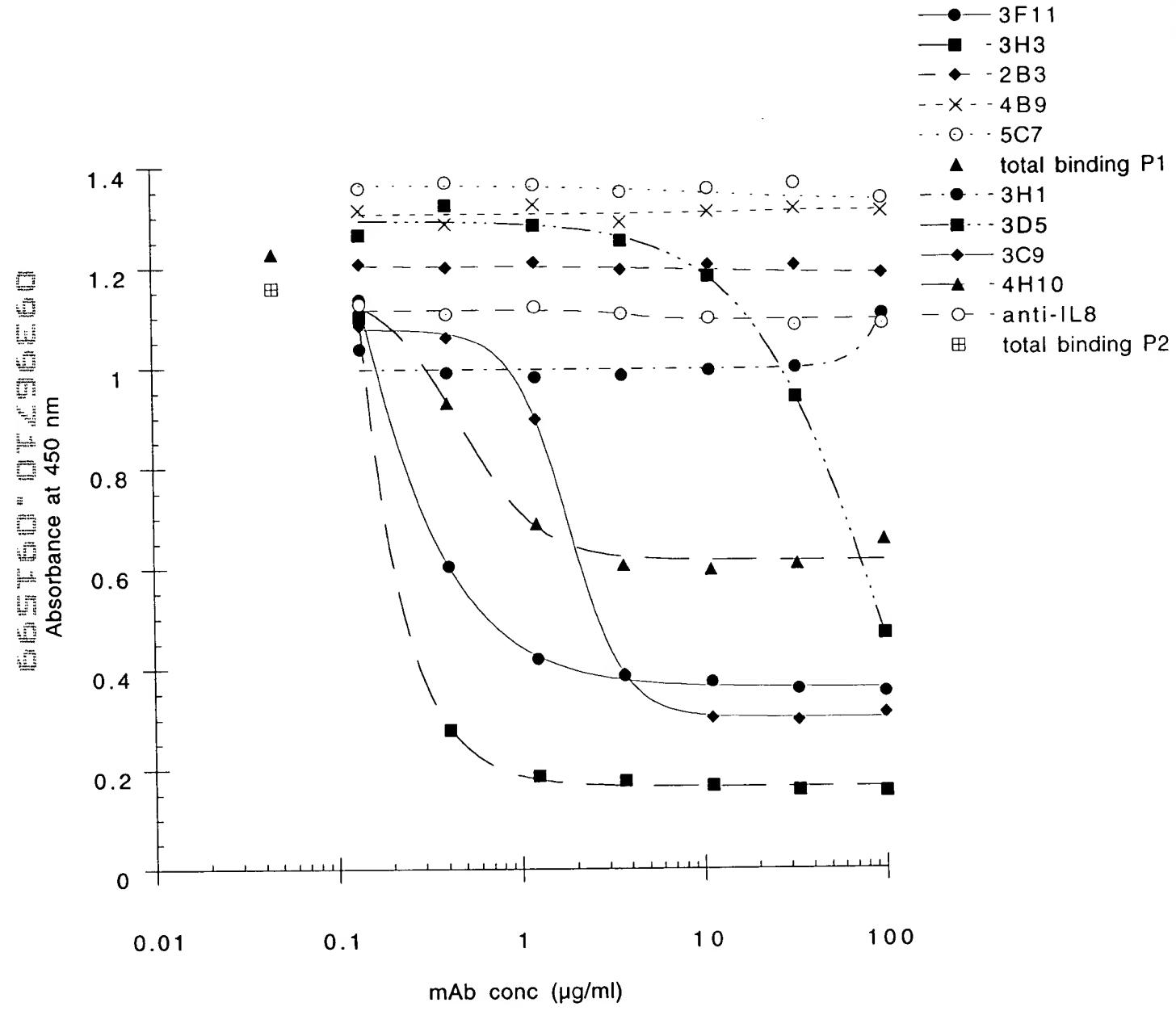
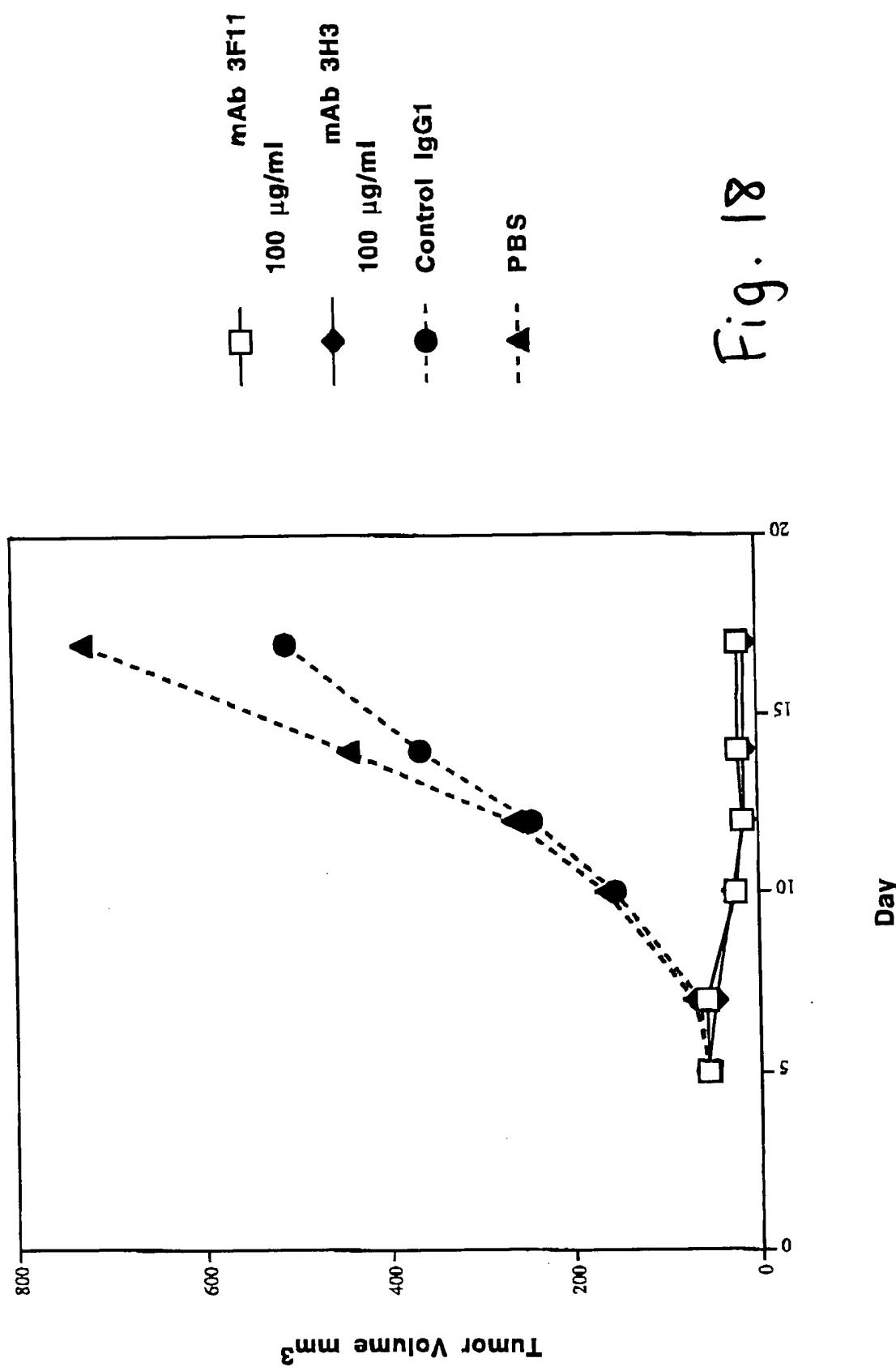


Fig. 17



Data Collection

	In-house	SSRL
Resolution (Å)	30–3.5 (3.62–3.50) ^a	30–2.4 (2.49–2.40) ^a
R _{sym} ^b	0.185 (0.398) ^a	0.056 (0.396) ^a
Number of observations	51,527	152,986
Unique reflections	12,459	38,908
Completeness (%)	99.8 (99.9) ^a	99.8 (99.7) ^a

Refinement

Resolution (Å)	30–2.4
Number of reflections	38,850
Final R ^c , R _{free} (F>0)	0.222, 0.267
Number of residues	781
Number of solvent molecules	286
Number of non-H atoms	6577
Average B factor (Å ²)	47.6
Rmsd bonds (Å)	0.013
Rmsd angles (°)	1.7
Rmsd B (bonded atoms) (Å ²)	2.4

^a Numbers in parentheses refer to the highest resolution shell.

^b R_{sym} = $\sum |I - \langle I \rangle| / \sum I$. $\langle I \rangle$ is the average intensity of symmetry related observations of a unique reflection.

^c R = $\sum |F_o - F_c| / \sum F_o$. R_{free} is calculated as R, but for 10% of the reflections excluded from all refinement.

Fig. 19

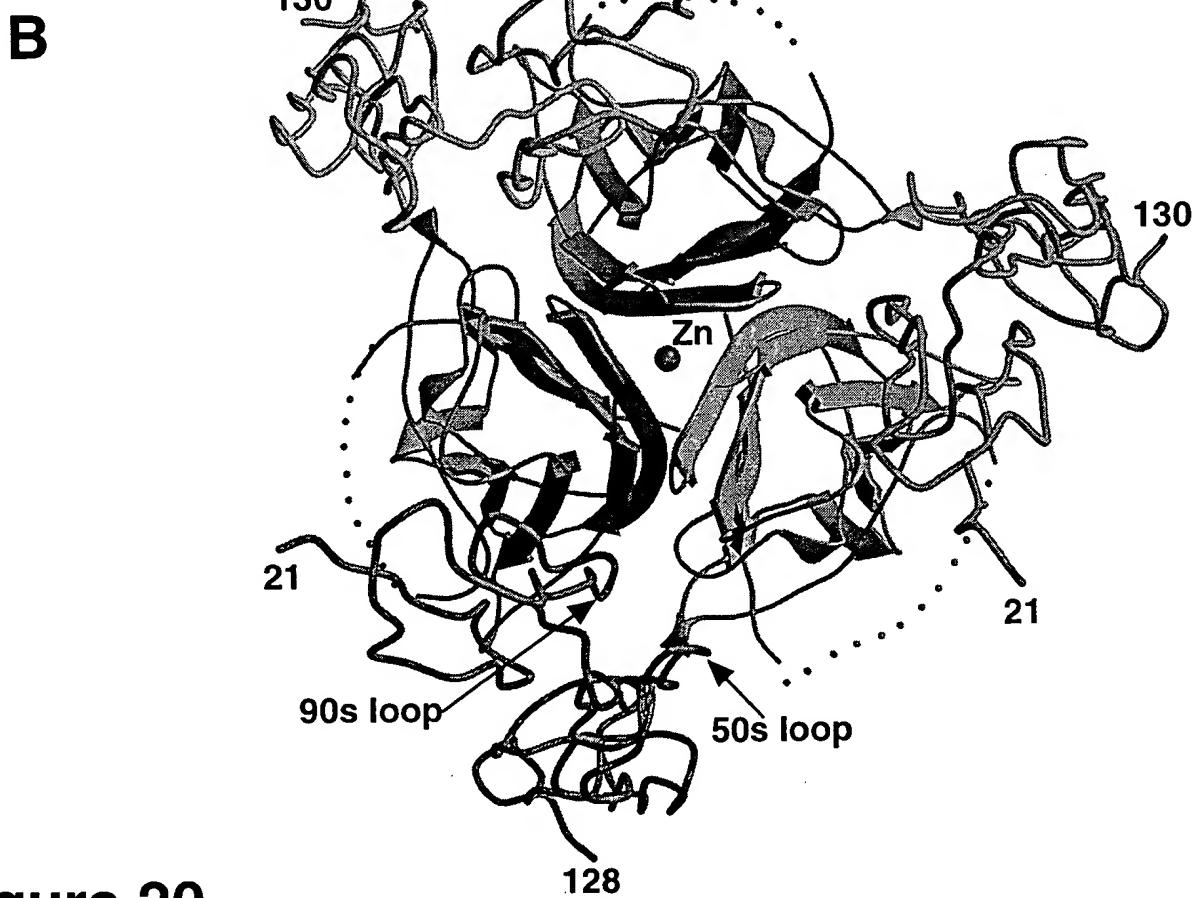
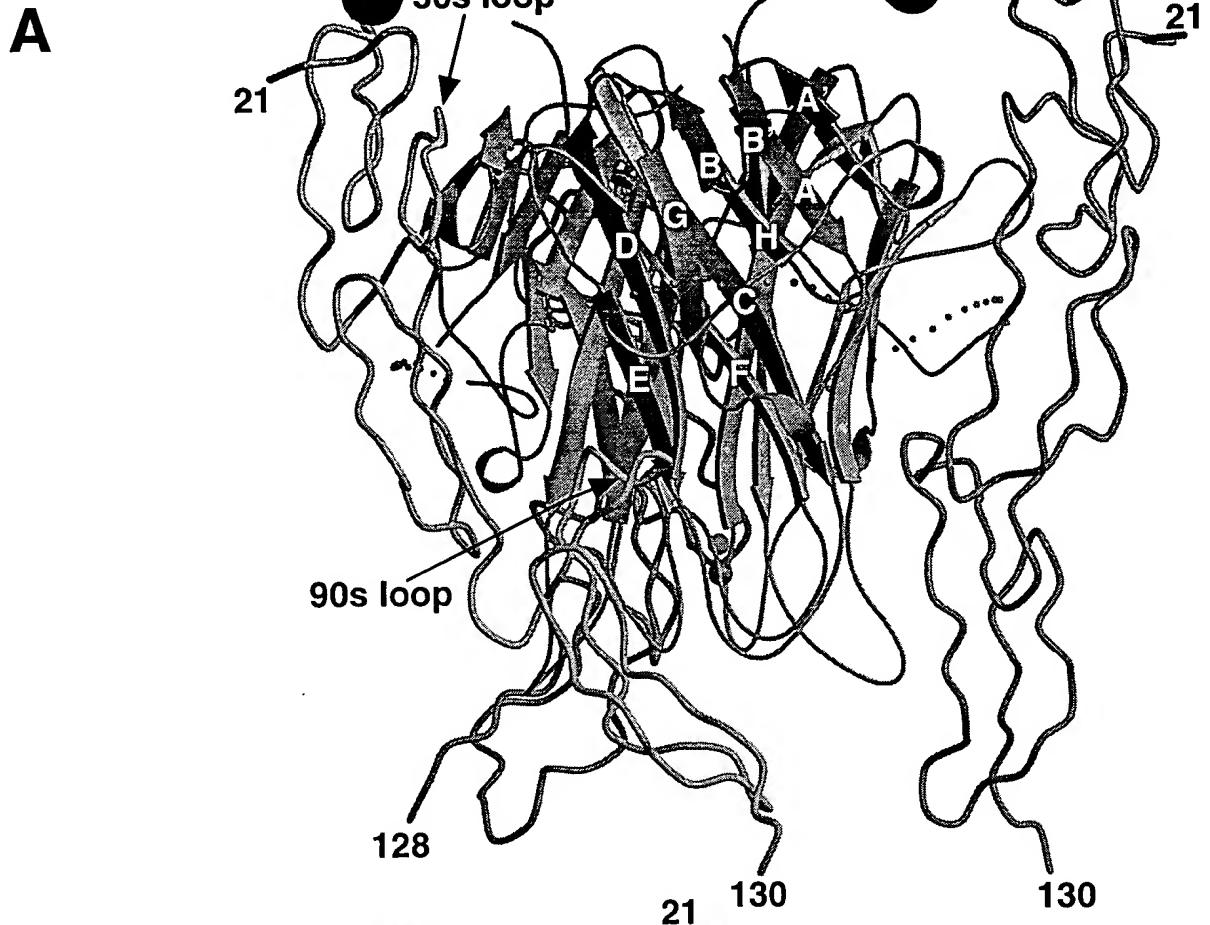


Figure 20

Figure 21

